



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 08/922,240  
Source: IFW16  
Date Processed by STIC: 7/23/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/efb/efs/downloads/documents.htm>) , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box-1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):  
U.S. Patent and Trademark Office, 220 20<sup>th</sup> Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Revised 05/17/04

## Raw Sequence Listing Error Summary

### ERROR DETECTED

### SUGGESTED CORRECTION

SERIAL NUMBER: 08/922,240

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1.      Wrapped Nucleics  
    Wrapped Aminos     The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
  
2.      Invalid Line Length     The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
  
3.      Misaligned Amino  
    Numbering     The numbering under each 5<sup>th</sup> amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.
  
4.      Non-ASCII     The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. Please **ensure your subsequent submission is saved in ASCII text**.
  
5.      Variable Length     Sequence(s)      contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
  
6.      PatentIn 2.0  
    "bug"     A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)     . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
  
7.      Skipped Sequences  
    (OLD RULES)     Sequence(s)      missing. If intentional, please insert the following lines for **each** skipped sequence:  
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
 (i) **SEQUENCE CHARACTERISTICS:** (Do not insert any subheadings under this heading)  
 (xi) **SEQUENCE DESCRIPTION:** SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
 This sequence is intentionally skipped  
  
 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.
  
8.      Skipped Sequences  
    (NEW RULES)     Sequence(s)      missing. If **intentional**, please insert the following lines for **each** skipped sequence.  
 <210> sequence id number  
 <400> sequence id number  
 000
  
9.      Use of n's or Xaa's  
    (NEW RULES)     Use of n's and/or Xaa's have been detected in the Sequence Listing.  
 Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.  
 In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.
  
10.      Invalid <213>  
    Response     Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species) <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence
  
11.      Use of <220>     Sequence(s)      missing the <220> "Feature" and associated numeric identifiers and responses.  
 Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
  
12.      PatentIn 2.0  
    "bug"     Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
  
13.      Misuse of n/Xaa     "**n**" can **only** represent a single nucleotide; "**Xaa**" can **only** represent a single amino acid



IFW16

## RAW SEQUENCE LISTING

DATE: 07/23/2004

PATENT APPLICATION: US/08/922,240

TIME: 13:24:42

Input Set : A:\APBI-P01-007.TXT

Output Set: N:\CRF4\07232004\H922240.raw

4 <110> APPLICANT: Schreiber, Stuart L.  
 5 Belshaw, Peter  
 6 Crabtree, Gerald R.  
 8 <120> TITLE OF INVENTION: GENE THERAPY BY CELL SPECIFIC TARGETING  
 11 <130> FILE REFERENCE: APBI-P01-007  
 13 <140> CURRENT APPLICATION NUMBER: US 08/922,240  
 14 <141> CURRENT FILING DATE: 1997-08-27  
 16 <150> PRIOR APPLICATION NUMBER: US 60/024,666  
 17 <151> PRIOR FILING DATE: 1996-08-27  
 19 <160> NUMBER OF SEQ ID NOS: 3  
 21 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
 23 <210> SEQ ID NO: 1  
 24 <211> LENGTH: 10  
 25 <212> TYPE: PRT  
 26 <213> ORGANISM: Unknown  
 28 <220> FEATURE:  
 29 <223> OTHER INFORMATION: Peptide  
 W--> 31 <221> NAME/KEY: VARIANT  
 32 <222> LOCATION: 1  
 33 <223> OTHER INFORMATION: Xaa = Abu: alpha-aminobutyric acid  
 W--> 35 <221> VARIANT  
 36 <222> LOCATION: 2  
 37 <223> OTHER INFORMATION: Xaa = Sar: sarcosine  
 W--> 39 <221> VARIANT  
 40 <222> LOCATION: 3, 5, 8, 9  
 41 <223> OTHER INFORMATION: Xaa = MeLeu: N-methyllleucine  
 W--> 43 <221> VARIANT  
 44 <222> LOCATION: 7  
 45 <223> OTHER INFORMATION: Xaa = D-Ala: D-alanine  
 W--> 47 <221> VARIANT  
 48 <222> LOCATION: 10  
 49 <223> OTHER INFORMATION: Xaa = Ac-N-MeValinol ester  
 W--> 51 <400> 1  
 W--> 52 Xaa Xaa Xaa Val Xaa Ala Xaa Xaa Xaa Xaa  
 53 1 5 10  
 56 <210> SEQ ID NO: 2  
 57 <211> LENGTH: 12  
 58 <212> TYPE: PRT  
 59 <213> ORGANISM: Unknown  
 61 <220> FEATURE:  
 62 <223> OTHER INFORMATION: Peptide  
 W--> 64 <221> NAME/KEY: VARIANT  
 65 <222> LOCATION: 1

pp1-3

Dec 10 1 10pm  
 07/23/04 13:24:42

understood - please attempt to give  
 (but insufficient)

source of genetic  
 material as explanation  
 for (213) Unknown  
 (see item 11 on  
 Error Summary  
 sheet)

same error

## RAW SEQUENCE LISTING

DATE: 07/23/2004

PATENT APPLICATION: US/08/922,240

TIME: 13:24:42

Input Set : A:\APBI-P01-007.TXT

Output Set: N:\CRF4\07232004\H922240.raw

66 <223> OTHER INFORMATION: Xaa = Fmoc-CpSar:  
67 9-fluorenylmethoxycarbonyl-cyclopentyl sarcosine  
W--> 69 <221> VARIANT  
70 <222> LOCATION: 2  
71 <223> OTHER INFORMATION: Xaa = MeBmt:  
72 (4R)-N-methyl-4-butenyl-4-methyl-L-threonine  
W--> 74 <221> VARIANT  
75 <222> LOCATION: 3  
76 <223> OTHER INFORMATION: Xaa = Abu: alpha-aminobutyric acid  
W--> 78 <221> VARIANT  
79 <222> LOCATION: 4  
80 <223> OTHER INFORMATION: Xaa = Sar: sarcosine  
W--> 82 <221> VARIANT  
83 <222> LOCATION: 5, 7, 10, 11  
84 <223> OTHER INFORMATION: Xaa = MeLeu: N-methyllleucine  
W--> 86 <221> VARIANT  
87 <222> LOCATION: (9)...(9)  
88 <223> OTHER INFORMATION: Xaa = D-Ala: D-alanine  
W--> 90 <221> VARIANT  
91 <222> LOCATION: (12)...(12)  
92 <223> OTHER INFORMATION: Xaa = Valinol ester  
W--> 94 <400> 2  
W--> 95 Xaa Xaa Xaa Xaa Xaa Val Xaa Ala Xaa Xaa Xaa Xaa  
96 1 5 10  
99 <210> SEQ ID NO: 3  
100 <211> LENGTH: 11  
101 <212> TYPE: PRT  
102 <213> ORGANISM: Unknown  
104 <220> FEATURE:  
105 <223> OTHER INFORMATION: Peptide  
W--> 107 <221> NAME/KEY: VARIANT  
108 <222> LOCATION: 1  
109 <223> OTHER INFORMATION: Xaa = Me-CpSar: methyl-cyclopentyl sarcosine  
W--> 111 <221> VARIANT  
112 <222> LOCATION: 2  
113 <223> OTHER INFORMATION: Xaa = MeBmt:  
114 (4R)-N-methyl-4-butenyl-4-methyl-L-threonine  
W--> 116 <221> VARIANT  
117 <222> LOCATION: 3  
118 <223> OTHER INFORMATION: Xaa = Abu: alpha-aminobutyric acid  
W--> 120 <221> VARIANT  
121 <222> LOCATION: 4  
122 <223> OTHER INFORMATION: Xaa = Sar: sarcosine  
W--> 124 <221> VARIANT  
125 <222> LOCATION: 5, 7, 10  
126 <223> OTHER INFORMATION: Xaa = MeLeu: N-methyllleucine  
W--> 128 <221> VARIANT  
129 <222> LOCATION: (11)...(11)  
130 <223> OTHER INFORMATION: Xaa = MeLeu-(OH): hydroxyl-N-methyllleucine

what about Xaa  
at location 9?  
(see p. 3)

RAW SEQUENCE LISTING

PATENT APPLICATION: US/08/922,240

DATE: 07/23/2004

TIME: 13:24:42

Input Set : A:\APBI-P01-007.TXT

Output Set: N:\CRF4\07232004\H922240.raw

W--> 132 <400> 3

W--> 133 Xaa Xaa Xaa Xaa Xaa Val Xaa Ala Xaa Xaa Xaa  
134 1 5 10

RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/08/922,240

DATE: 07/23/2004  
TIME: 13:24:43

Input Set : A:\APBI-P01-007.TXT  
Output Set: N:\CRF4\07232004\H922240.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; Xaa Pos. 1,2,3,5,7,8,9,10  
Seq#:2; Xaa Pos. 1,2,3,4,5,7,8,10,11,12  
Seq#:3; Xaa Pos. 1,2,3,4,5,7,9,10,11

## VERIFICATION SUMMARY

DATE: 07/23/2004

PATENT APPLICATION: US/08/922,240

TIME: 13:24:43

Input Set : A:\APBI-P01-007.TXT

Output Set: N:\CRF4\07232004\H922240.raw

L:31 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!  
L:35 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1  
L:39 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1  
L:43 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1  
L:47 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1  
L:51 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1  
L:52 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0  
L:64 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!  
L:69 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2  
L:74 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2  
L:78 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2  
L:82 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2  
L:86 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2  
L:90 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2  
L:94 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2  
L:95 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:0  
L:107 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!  
L:111 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3  
L:116 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3  
L:120 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3  
L:124 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3  
L:128 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3  
L:132 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3  
L:133 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0